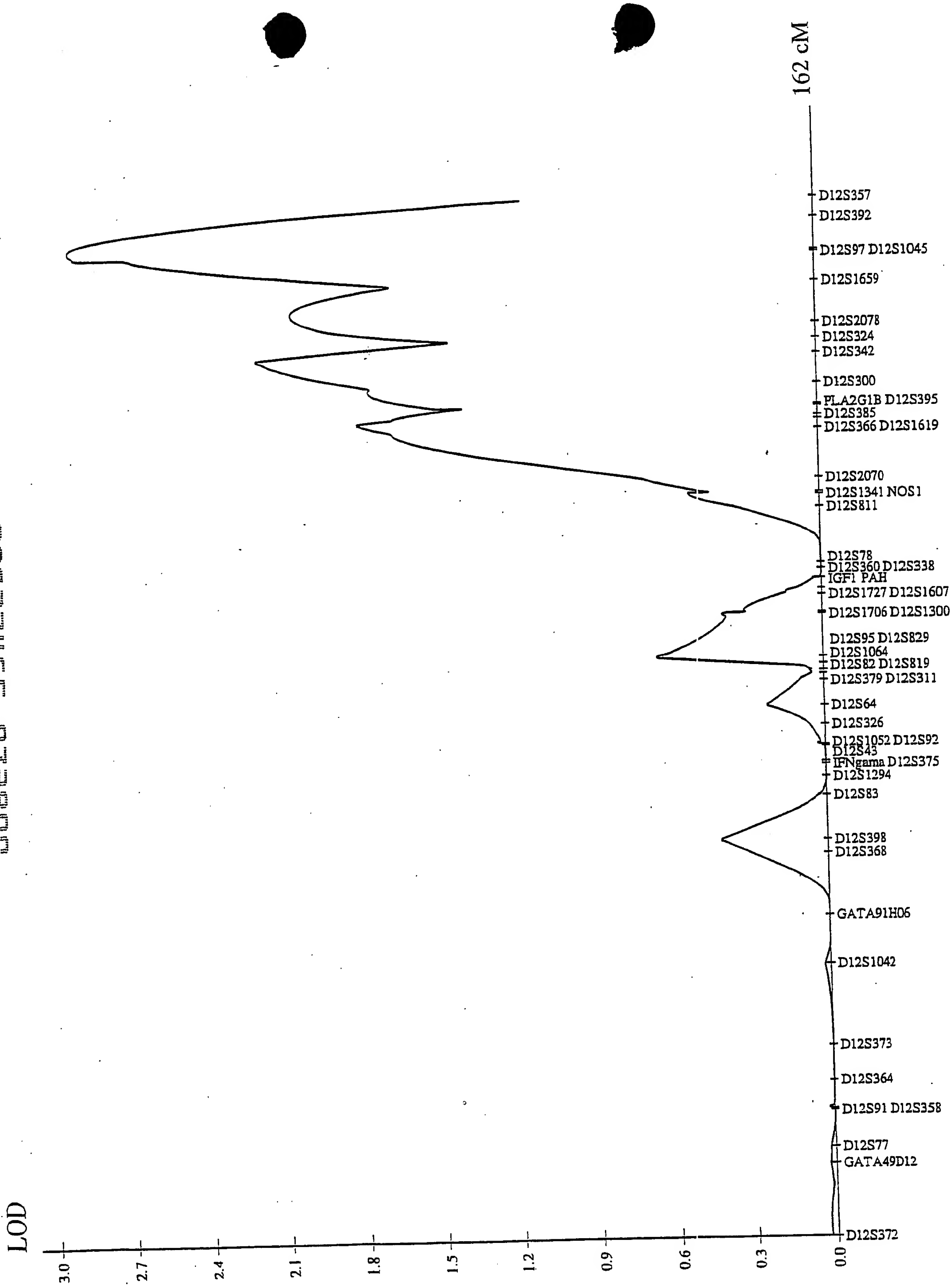
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D12S342
D12S300
PLA2G1B D12S395
D12S385
D12S366 D12S1619
D12S2070
D12S1341 NOS1
D12S811
D12S78
D12S360 D12S338
IGF1 PAH
D12S1727 D12S1607
D12S1706 D12S1300
D12S95 D12S829
D12S1064
D12S82 D12S819
D12S379 D12S311
D12S64
D12S326
D12S1052 D12S92
D12S43
IFNgama D12S375
D12S1294
D12S83
D12S398
D12S368
GATA91H06
D12S1042
D12S373
D12S364
D12S91 D12S358
D12S77
GATA49D12
D12S372
LOD
3.0
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
0.0

Figure 1

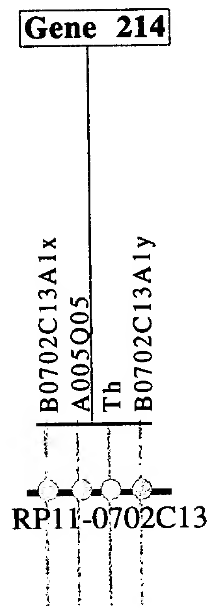


Figure 2

```
        10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
 T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                 110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
 S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

       130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
 H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

       190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
 L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

       250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
 V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

       310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
 P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

       370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
 R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

       430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

       490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
 P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 3A

```
         550                 570                 590
           .         .         .         .         .         .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

         610                 630                 650
           .         .         .         .         .         .
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
 T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

         670                 690                 710
           .         .         .         .         .         .
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
 H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

         730                 750                 770
           .         .         .         .         .         .
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
 D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

         790                 810                 830
           .         .         .         .         .         .
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
 A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

         850                 870                 890
           .         .         .         .         .         .
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
 G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

         910                 930                 950
           .         .         .         .         .         .
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
 S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

         970                 990                1010
           .         .         .         .         .         .
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
 L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

        1030                1050                1070
           .         .         .         .         .         .
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
 G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 3B

```
      1090                1110                1130
         .         .         .         .         .
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
 A  P  R  C  A  A  L  D  L  P  P  W  T  W  E  P  P  G  S  S

      1150                1170                1190
         .         .         .         .         .
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCT
 H  S  G  K  E  G  S  G  H  G  G  R  P  G  P  I  P  V  P  W

      1210                1230                1250
         .         .         .         .         .
GGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC
 P  F  F  L  L  P  V  C  H  C  P  G  A  F  A  P  A  F  P  L

      1270                1290                1310
         .         .         .         .         .
TCTCTAGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGA
 S  R  Q  G  F  S  S  L  A  R  L  V  S  N  S  *

      1330                1350                1370
         .         .         .         .         .
TCCACCTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCC

      1390                1410                1430
         .         .         .         .         .
ATCATTCCTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCAC

      1450                1470                1490
         .         .         .         .         .
TCATCAGTTGATGGTCATGTGGGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGA

      1510                1530                1550
         .         .         .         .         .
ATAAACGTTCCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAACTGCTGGGTCAAAAAA

      1570
         .         .
AAAAAAAAAAAAAAAAAAAA
```

Figure 3C

```
        10                30                50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
 T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                90               110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
 S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

       130               150               170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
 H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

       190               210               230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
 L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

       250               270               290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
 V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

       310               330               350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
 P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

       370               390               410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
 R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

       430               450               470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

       490               510               530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
 P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P

       550               570               590
```

Figure 4A

CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
R P L Q E G T R V H E L P T R S P G G D

610 630 650

ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
T G F T S C P R P L Q E G T P G S R A A

670 690 710

CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
H V L S R R G H R V H E L P T S S P G G

730 750 770

GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
D T G F T S C P R P L Q E G T P G S R A

790 810 830

CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
A H V L S R K G P G S T S C P R P L Q E

850 870 890

AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
G T P G S R A A H A L S R K G P R V Q V

910 930 950

TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
S C R P T S C L C V N Q K K D E E Q A L

970 990 1010

TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
L S L Q A G F G G G A G S P A A P S L A

1030 1050 1070

CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
G H P V L E P Q N C R R P A E K G S M M

1090 1110 1130

TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGAGACAGGGTTTCTCCT
A P R C A A L D L P P W T W R Q G F S S

Figure 4B

1150 1170 1190

CATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGATCCACCTGCCTCAGCCTCCCG
L A R L V S N S *

1210 1230 1250

AAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCCATCATTCCTTTTTACTGCTGA

1270 1290 1310

CTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCACTCATCAGTTGATGGTCATGTG

1330 1350 1370

GGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGAATAAACGTTCCTGTGCACTCT

1390 1410 1430

TGGGCATACGCCTAGGAGTGGAACTGCTGGGTCAAAAAAAAAAAAAAAAAAAAAAAAAAA

A

Figure 4C

```
        10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
 T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                 110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
 S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

       130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
 H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

       190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
 L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

       250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
 V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

       310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
 P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

       370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
 R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

       430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

       490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
 P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 5A

```
     550                 570                 590
      .         .         .         .         .         .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
  R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

     610                 630                 650
      .         .         .         .         .         .
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

     670                 690                 710
      .         .         .         .         .         .
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
  H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

     730                 750                 770
      .         .         .         .         .         .
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
  D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

     790                 810                 830
      .         .         .         .         .         .
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
  A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

     850                 870                 890
      .         .         .         .         .         .
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
  G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

     910                 930                 950
      .         .         .         .         .         .
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
  S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

     970                 990                1010
      .         .         .         .         .         .
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
  L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

    1030                1050                1070
      .         .         .         .         .         .
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
  G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 5B

```
       1090                1110                1130
          .         .         .         .         .         .
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
  A  P  R  C  A  A  L  D  L  P  P  W  T  W  E  P  P  G  S  S

       1150                1170                1190
          .         .         .         .         .         .
CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGCTTTATTGAGGTATAGTTGACAATTCA
  H  S  G  K  E  G  S  G  H  G  A  L  L  R  Y  S  *

       1210                1230                1250
          .         .         .         .         .         .
GGACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAAT

       1270                1290                1310
          .         .         .         .         .         .
GAGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTG

       1330                1350                1370
          .         .         .         .         .         .
GTGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGT

       1390                1410                1430
          .         .         .         .         .         .
CTCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACT

       1450                1470                1490
          .         .         .         .         .         .
TGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCA

       1510                1530                1550
          .         .         .         .         .         .
GCCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATC

       1570
          .
AAAAAAAAAAAAAAAA
```

Figure 5C

```
        10                  30                  50
         .         .         .         .         .         .
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
 T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

        70                  90                 110
         .         .         .         .         .         .
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
 S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

       130                 150                 170
         .         .         .         .         .         .
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
 H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

       190                 210                 230
         .         .         .         .         .         .
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
 L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

       250                 270                 290
         .         .         .         .         .         .
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
 V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

       310                 330                 350
         .         .         .         .         .         .
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
 P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

       370                 390                 410
         .         .         .         .         .         .
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
 R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

       430                 450                 470
         .         .         .         .         .         .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

       490                 510                 530
         .         .         .         .         .         .
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
 P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 6A

```
         550                 570                 590
          .         .         .         .         .         .
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

         610                 630                 650
          .         .         .         .         .         .
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
 T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

         670                 690                 710
          .         .         .         .         .         .
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
 H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

         730                 750                 770
          .         .         .         .         .         .
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
 D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

         790                 810                 830
          .         .         .         .         .         .
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
 A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

         850                 870                 890
          .         .         .         .         .         .
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
 G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

         910                 930                 950
          .         .         .         .         .         .
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
 S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

         970                 990                1010
          .         .         .         .         .         .
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
 L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

        1030                1050                1070
          .         .         .         .         .         .
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
 G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 6B

1090 1110 1130

TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGATGCCAGTGATGCCTG
A P R C A A L D L P P W T W M P V M P E

1150 1170 1190

AGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGGAGCCTGTGCTTGACCC
V C R A V H T L T A W P L R S L C L T P

1210 1230 1250

CCAAATCCGCCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCATGAGGGGCCTTCCCCA
K S A P Q L P V T G S L L P *

1270 1290 1310

GGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGCAGAGTGCTGCCCCCGCCTGCCC

1330 1350 1370

ACCTGGCCTGGACCCTCGCCTGAGCCCCCTCAGGGCTCTGCGCCACCTCAACCCAGGCGT

1390 1410 1430

TTGTTCCGCAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

1450 1470 1490

GTCGGCCAGGCCCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCC

1510 1530 1550

CCGGGGCCTTTGCACCTGCATTCCCTCTCTCTGTGAGTGTCCTGGGGCCCGTTACCCACG

1570 1590 1610

TCACCGTCCCAGGATACCTTTTCTTTTCTTTCTCTCTCTCCAGCTTTATTGAGGTATAGT

1630 1650 1670

TGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGC

1690 1710 1730

ATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACT

Figure 6C

1750 1770 1790

TCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGT

1810 1830 1850

GAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGT

1870 1890 1910

CCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCG

1930 1950 1970

GTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACA

1990 2010

CATTCTTATCAAAAAAAAAAAAAAAAAAAA

Figure 6D

```
           10                  30                  50
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
 T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A  H  V  V

           70                  90                 110
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
 S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E  R  T  R  V

          130                 150                 170
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
 H  E  L  A  T  S  S  A  G  R  D  P  G  S  T  S  C  P  R  P

          190                 210                 230
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
 L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  K  G  P  R

          250                 270                 290
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
 V  H  E  L  P  T  S  S  P  G  R  D  P  G  S  T  N  C  P  R

          310                 330                 350
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
 P  L  Q  E  G  T  P  G  S  R  A  A  H  V  L  S  R  R  G  H

          370                 390                 410
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
 R  V  H  E  L  P  T  P  S  P  G  R  D  P  G  F  M  S  C  P

          430                 450                 470
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  P  S  P  G  G  D

          490                 510                 530
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
 P  G  P  R  A  A  H  V  V  N  G  K  G  P  G  S  T  S  C  P
```

Figure 7A

```
550                 570                 590
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
 R  P  L  Q  E  G  T  R  V  H  E  L  P  T  R  S  P  G  G  D

610                 630                 650
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
 T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A  A

670                 690                 710
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
 H  V  L  S  R  R  G  H  R  V  H  E  L  P  T  S  S  P  G  G

730                 750                 770
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
 D  T  G  F  T  S  C  P  R  P  L  Q  E  G  T  P  G  S  R  A

790                 810                 830
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
 A  H  V  L  S  R  K  G  P  G  S  T  S  C  P  R  P  L  Q  E

850                 870                 890
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
 G  T  P  G  S  R  A  A  H  A  L  S  R  K  G  P  R  V  Q  V

910                 930                 950
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
 S  C  R  P  T  S  C  L  C  V  N  Q  K  K  D  E  E  Q  A  L

970                 990                 1010
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
 L  S  L  Q  A  G  F  G  G  G  A  G  S  P  A  A  P  S  L  A

1030                1050                1070
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
 G  H  P  V  L  E  P  Q  N  C  R  R  P  A  E  K  G  S  M  M
```

Figure 7B

1090 1110 1130

TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGGGAACCTCCCGGCTCTT
A P R C A A L D L P P W T W E P P G S S

1150 1170 1190

CCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCT
H S G K E G S G H G G R P G P I P V P W

1210 1230 1250

GGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTC
P F F L L P V C H C P G A F A P A F P L

1270 1290 1310

TCTCTGTGAGTGTCCTGGGGCCCGTTACCCACGTCACCGTCCCAGGATACCTTTTCTTTT
S V S V L G P V T H V T V P G Y L F F S

1330 1350 1370

CTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAA
F S L S S F I E V *

1390 1410 1430

GGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGC

1450 1470 1490

TAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTT

1510 1530 1550

TAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAA

1570 1590 1610

AATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGG

1630 1650 1670

AGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGG

Figure 7C

1690 1710 1730

AGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATCAAAAAAAAAAAAAAAAA

AAAA

Figure 7D

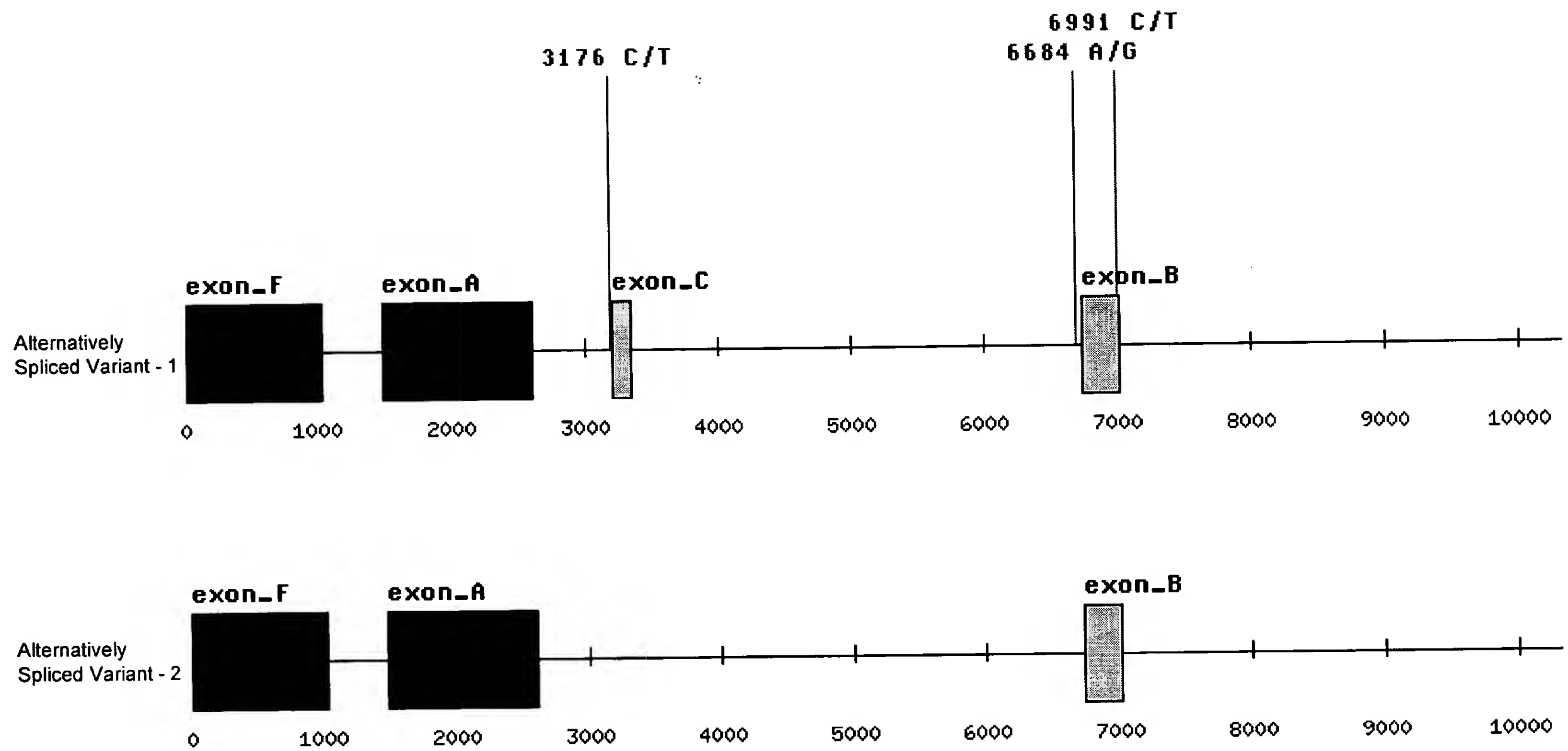
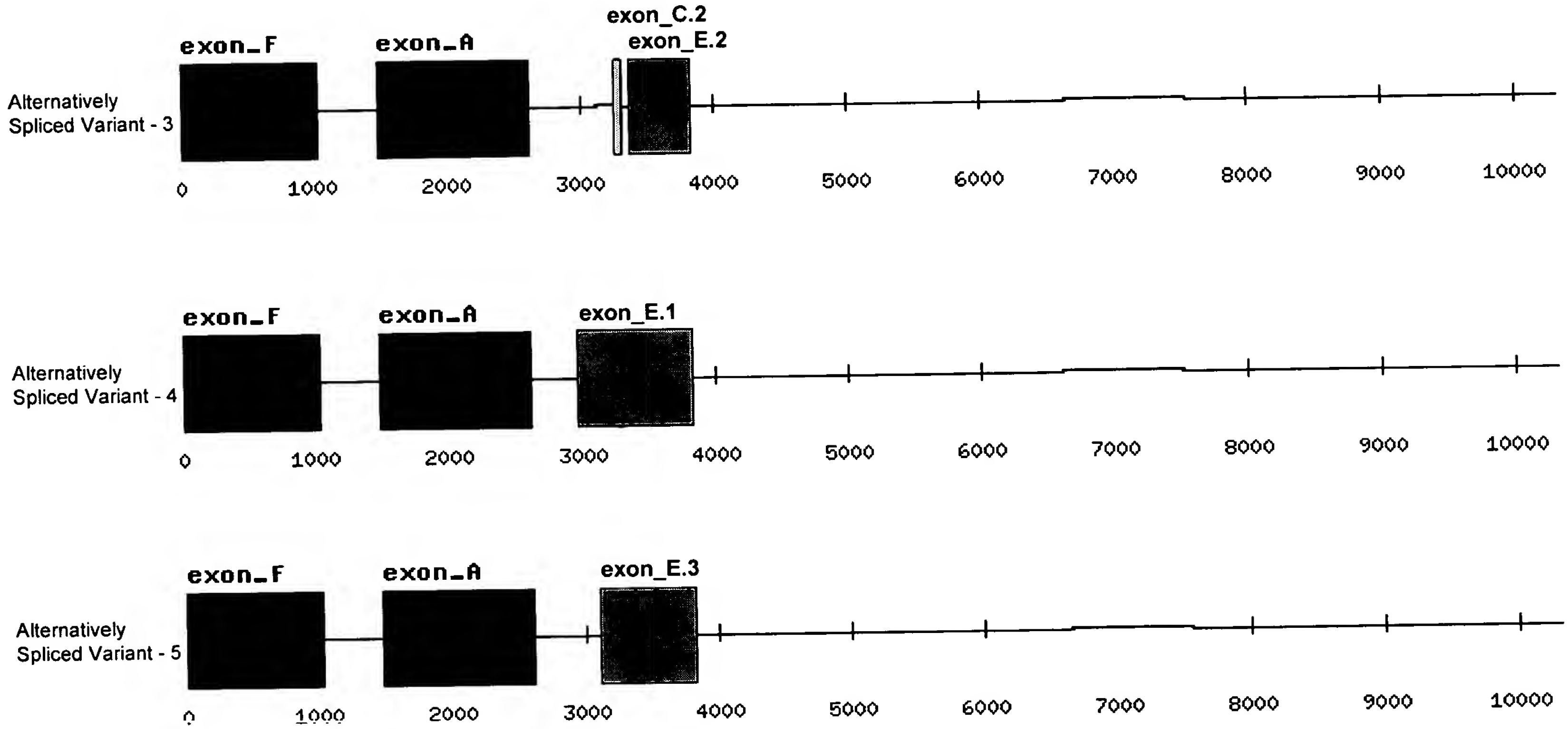


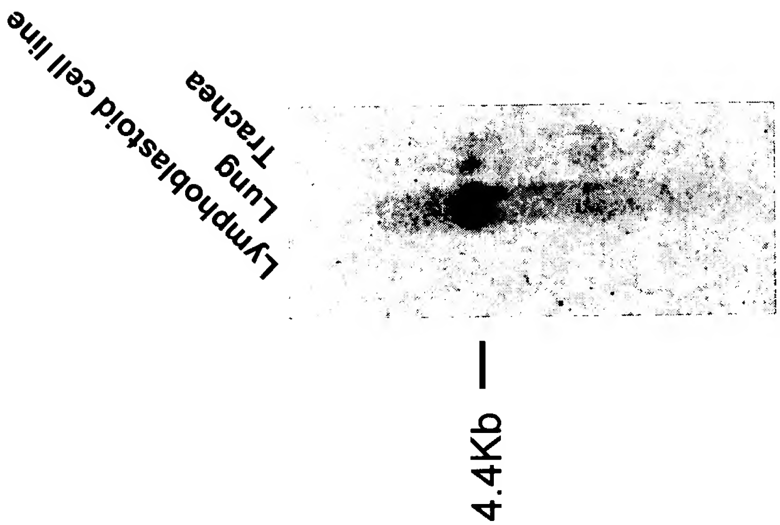
Figure 8A

Alternatively Spliced Variants from Gene 214



Alternatively Spliced Variants from Gene 214

Figure 8B



Northern blot analysis of Gene 214

Figure 9

>Gene 214 Exon_A
TCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCG
TCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAAGGACCCGGG
TCCACGAGCTGGCCACGTCCTCTGCAGGAAGGGACCCCGGGTCCACGAGCTGCCCACGTC
CTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCC
GGGTCCACGAGCTGCCCACGTCCTCTCCAGGAAGGGACCCCGGGTCCACGAACTGCCCAC
GTCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAGGGGAC
ACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCATGAGCTGCC
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCCCTCTCCAGGAGGGG
ACCCGGGTCCACGAGCTGCCCACGTCGTCAACGGGAAGGGACCCGGGTCCACGAGCTGCC
CACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAACTGCCCACGCGCTCTCCAGGAGGGG
ACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAAGGGACCCCGGGTTCACGAGCTG
CCCACGTCCTCTCCAGGAGGGGACACCGGGTTCACGAGCTGCCCACGTCCTCTCCAGGAG
GGGACACCGGGTTCACGAGCTGCCCACGCCCTCTCCAGGAGGGGACACCGGGTTCACGAG
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
AGGGGACACCGGGTTCACGAGCTGCCCACGCACTTTCCAGGAAGGGACCCCGGGTTCAGG
TCTCCTGCCGGCCCACATCGTGCCTTTGTGTAAATCAGAAGAAAGATGAGGAACAGGCCC
TCCTCTCTCTCCAGGCAGGCTTTGGTGGAGGGGCTGGATCTCCTGCCGCACCTTCCCTGG
CAGGGCACCCTGTGCTTGAGCCCCAGAACTGCAGGCGGCCGGCAGAGAAGGGGTCCATGA
TGGCGCCTCGGTGCGCAGCCTTGGACCTGCCCCCATGGACCTGG

>Gene 214 Exon_B
AGACAGGGTTTCTCCTCATTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGACGATCCAC
CTGCCTCAGCCTCCCGAAGTGTTGGGATTACAGGCACGAGCCACTGTGCCCGGCCATCAT
TCCTTTTTACTGCTGACTAATAGTCTGCTGTGTGAATCCACCGCTAGAAACCCACTCATC
AGTTGATGGTCATGTGGGTTGCTTCTGCTATTCGCTTATTATGAACAGTGCTGGAATAAA
CGTTCCTGTGCACTCTTGGGCATACGCCTAGGAGTGGAACTGCTGGGTC

>Gene 214 Exon C
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGC
CCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTT
GCACCTGCATTCCCTCTCTCT

>Gene 214 Exon C.2
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAG

>Gene 214 Exon E.1
ATGCCAGTGATGCCTGAGGTCTGCAGGGCAGTGCATACGCTCACCGCCTGGCCGCTCAGG
AGCCTGTGCTTGACCCCCAAATCCGCCCCCCAACTCCCTGTTACCGGCTCACTCCTTCCA
TGAGGGGCCTTCCCCAGGGACAGCCGATGCTCTCCTGATGGCTCCTGCCCTTGCAGAGTG
CTGCCCCCGCCTGCCCACCTGGCCTGGACCCTCGCCTGAGCCCCCTCAGGGCTCTGCGCC
ACCTCAACCCAGGCGTTTGTTCCGCAGGAACCTCCCGGCTCTTCCCACTCGGGAAAGGAA
GGCTCTGGGCATGGAGGTCGGCCAGGCCCCATCCCCGTACCCTGGCCCTTCTTCCTGCTT
CCTGTTTGTCACTGCCCCGGGGCCTTTGCACCTGCATTCCCTCTCTCTGTGAGTGTCCTG
GGGCCCGTTACCCACGTCACCGTCCCAGGATACCTTTTCTTTTCTTTCTCTCTCTCCAGC
TTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACAA
CCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCATC
ACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACACA
GCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGGT
GGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCTG
GGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAAT
AAATAAATAAAGGACACATTCTTATC

FIGURE 10A

>Gene 214 Exon E.2
CTTTATTGAGGTATAGTTGACAATTCAGGACGGTGTGCACTCAAGGTATGCAGCATCACA
ACCTGACACACGTAGGCATTGTGAAATGAGTCCCACAATTGGGCTAATTAACACACCCAT
CACCTTACATGGTTACTTCTTTCTGTGGTGAGAACACTAAATTTTAAATAGAGGACACAC
AGCCTGGGCAACATAGTGAGACCCTGTCTCTACAAATATAAAAAAATTATCTGGACGTGG
TGGTGCACACCTGTGGTCCCAGCTACTTGGGAAGCTGAGGCTGGAGAATCACTTGAGCCT
GGGAGGCGGAGGTTGCGGTGCACTCCAGCCTGGGCGACAGAGGGAGGCCCTATCTCAAAA
TAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon E.3
GAACCTCCCGGCTCTTCCCACTCGGGAAAGGAAGGCTCTGGGCATGGAGGTCGGCCAGGC
CCCATCCCCGTACCCTGGCCCTTCTTCCTGCTTCCTGTTTGTCACTGCCCCGGGGCCTTT
GCACCTGCATTCCCTCTCTCTGTGAGTGTCCTGGGGCCCGTTACCCACGTCACCGTCCCA
GGATACCTTTTCTTTTCTTTCTCTCTCTCCAGCTTTATTGAGGTATAGTTGACAATTCAG
GACGGTGTGCACTCAAGGTATGCAGCATCACAACCTGACACACGTAGGCATTGTGAAATG
AGTCCCACAATTGGGCTAATTAACACACCCATCACCTTACATGGTTACTTCTTTCTGTGG
TGAGAACACTAAATTTTAAATAGAGGACACACAGCCTGGGCAACATAGTGAGACCCTGTC
TCTACAAATATAAAAAAATTATCTGGACGTGGTGGTGCACACCTGTGGTCCCAGCTACTT
GGGAAGCTGAGGCTGGAGAATCACTTGAGCCTGGGAGGCGGAGGTTGCGGTGCACTCCAG
CCTGGGCGACAGAGGGAGGCCCTATCTCAAAATAAATAAATAAAGGACACATTCTTATC

>Gene 214 Exon F
CGGGCGTGTATATCTCTTCATAGAGAGCGCTCAGACAGCGTGCGTTAATCTGCGTCGATA
TATAGAGATCTTTATCACTGAGTAGATAGAACGTACATGAATGTACGAACAGTCCAGACG
AGTAACTTGACTAGGATAAGATAGACAGTACCAACTAATGAGACAAGAAGAGGGAATCAT
ATAGAATCATGTAGTCTGAGTCTAGCGAGTGTCGACATGATCACAAGCGAAATACAGACT
ATGAGAAGAGGTAGAAATAATAAGTANACTGAGAAGAGAGGTCATATGTACATACAAATC
AGTAAAGCAATAGAAATTGAATACATTATAAGCCACAGTTACAGAATTAGCCTAATTTAA
CAACCATGGCAAGCGAGTTATATCAAACATAGAAGAGTAAACTCTATCGACCATGGGTAG
GAACGAATAAAGGCGTCGAGAAGACAATAAGAATGCGTGTTAAACAGCAATACAAGAGAA
TAGCACCACTGAAGCAGACCAAAGGCGTCACCGGGGAAGTAGGGAAGAGGCACCTCACAA
GGAGAGGAAAGGGCAGTCCTGATTTTGAAAATTTCAGTGAAAAGACAGTGTTGTTCCCGG
AGGCAGCTTAGTGATCCCGCATCGACTCTGAAGAGGACCCTGAGGGTAGGGGATTTTTGG
GCCTGACCGGCCTATGCTGAACGCCCACCGGGAATTCAGGGAGAAACACGGGGCCCCGGC
TTCCAGGAGAGCAGCCAGGCCACAGCCCTGAGGACGGGCAAACCCCACCCAGGCACGGTG
AGAGGGAGGCCGCCCAGGCCTGGGGCCTGGCGGCAGGGGATGAAGTGGACCAGAGCCCCG
CAAATCCTAACGTGGGTGAGCAGTGAGCCTGTGTGGCTGCGAGTGGCTCCGTTTTGGGGC
TGTTTGTTCCTGCAGCAAATGATGCCAGCCCTGACGGAACCAGTGCACGTCCACCACGAG
CTGCCCACGTCCTCTCCAGGAAGGGACCCGGGTCCACGAGCTGCCCACGTCCTCTCCAGG
AAGGGACC

FIGURE 10B